February 10, 2005 as International Publication No. WO 2005/013091 (the "International Application"). This application also claims priority from U.S. Patent Application Serial No. 60/492,210, filed on August 1, 2003 (the "'210 Application"). The~~, the~~ entire disclosures of these applications are ~~which~~ incorporated herein by reference. This application claims priority from the International Application pursuant to 35 U.S.C. § 365, and from the '210 Application pursuant to 35 U.S.C. §§ 119(e) and 365.--.

IN THE CLAIMS:

Please cancel claims 22-40, 42-60 and 62-80, without prejudice. In addition, please amend claims 4-6, and add new claim 81, as provided below. The status of the claims pending in this application is provided in the associated claim listing on separate sheets:

1. (Original) A method for at least one of genotyping and haplotyping a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample, comprising:

   i) providing one or more microarrays that include a set of oligonucleotide probes that are capable of detecting the at least one of the genotypes and the haplotypes or the strain variant;

   ii) hybridizing the DNA sample to the one or more microarrays to create a hybridization pattern; and

   iii) determining at least one of a genotype and a haplotype or a strain variant based on the hybridization pattern.

2. (Currently Amended) The method of claim 1, wherein the one or more microarrays include a set of oligonucleotide probes that are capable of detecting at least one of all known genotypes or ~~and~~ all known haplotypes at the polymorphic genetic loci or the strain identification.

3. (Original) The method of claim 1, wherein the one or more microarrays are configured to include at least one of an optimal set and an optimal arrangement of oligonucleotide probes.

4~~.~~ (Currently Amended) The method of claim 1~~3~~, further comprising optimizing the least one of the set or ~~and~~ an arrangement of the oligonucleotide~~s~~ probes as a function of at least one of a match criteria and a mismatch criteria between the

true allelle contained in the DNA sample and the allele determined by the hybridizing step ~~the following:~~

$$\frac{\min \sum_{type\ j} w_j \; E\left[\Pi_{T_j \neq \hat{T}_j}\right]}{\Leftrightarrow \;\; \min \sum_{type\ j} w_j \; \Pr\left(T_j \neq \hat{T}_j\right).}$$

~~wherein T_j is a true allele contained in the DNA sample, $\hat{T}_j$ is the allele determined by the hybridization step, $\Pi_X = \begin{Bmatrix} 1, & \text{if } X \text{ is true} \\ 0, & \text{otherwise} \end{Bmatrix}$, and w_j is a weight assigned to at least one of the genotype and the haplotype j.~~

5. (Currently Amended) The method of claim 8~~14~~, wherein the weights are provided as follows: $w_j = 1 \forall_j$, wherein $\forall_j$ is a set of at least one of all known genotypes or ~~and~~ all known haplotypes at one or more predetermined polymorphic genetic loci.

6. (Currently Amended) The method of claim 8~~14~~, wherein the weights are provided as follows: w_j is different for each genotype or haplotype.

7. (Original) The method of claim 4, wherein step (iii) produces a vector of *n* measurements, wherein *n* is a number of probes contained on the one or more microarrays.

8. (Original) The method of claim 7, wherein the *n* potential probes provided to identify *N* known genotypes or haplotypes are each associated with a response vector $\vec{\upsilon}_j \in \{0,1\}^N, j = 1,\ldots,n.$

9. (Original) The method of claim 8, further comprising generating a graph *G* on vertices corresponding to probe response vectors.

10. (Original) The method of claim 9, wherein the graph *G* is a complete edge-weighted and vertex-weighted undirected graph *G* = (*V*, *E*) provided on *n* vertices, wherein *n* is the number of potential probes.

11. (Original) The method of claim 10, wherein the weights *w* of each vertex *v* and each edge *e* are constrained by: $0 \le w(v), w(e) \le 1$.

12. (Original) The method of claim 11, wherein the weight *w* of a vertex *v* is set to:

    w(*v*) = min{fraction of 0's, fraction of 1's}.

13. (Original) The method of claim 11, wherein the weight *w* of an edge *e* ={*u*,*v*} is set to:

    w(e) = Hamming distance/vector length,

    wherein Hamming distance is measured between the probe response vectors corresponding to vertices *u* and *v*, and vector length is the length of said probe response vectors, namely, *N*.

14. (Original) The method of claim 10, further comprising modifying the graph G by thresholding the edges such that the modified graph G_{mod} is defined as $G_{mod} = (V, E_{mod})$, wherein $E_{mod} = \{e \in E: w(e) \leq \rho\}$, and ρ is a selected threshold value.

15. (Original) The method of claim 14, wherein, for the modified graph G_{mod} and the probe set size M, the following is performed:

i) initializing a current-best list of independent sets with associated information weights,

ii) initializing vertex boosting weights to vertex weights $w(v)$,

iii) defining a probability distribution on the vertex subset based on vertex boosting weights,

iv) choosing a random subset of vertices of a specified size M based on the probability distribution,

v) eliminating one of the end-point vertices in each of the edges remaining in the induced subgraph on the random subset,

vi) modifying the vertex boosting weights by increasing the weights of the vertices that are retained in the subset and decreasing the weights of the vertices that were selected in step (iv) but eliminated in step (v), and

vii) repeating steps (iii) through (vi) for at least one of a predetermined number of iterations and until no improvement to the list of top independent sets is achieved.

16. (Original) The method of claim 15, wherein, for the modified graph G_{mod} and the probe set size M, steps (ii) through (vii) are repeated for a predetermined number of iterations, each iteration starting with reinitializing vertex boosting weights to vertex weights $w(v)$ in step (ii).

17. (Original) The method of claim 16, wherein, for a given fixed small $0<\epsilon<<1$, the probe set size M satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq 1) > 1-\epsilon$.

18. (Original) The method of claim 16, wherein, for a given fixed small $0<\epsilon<<1$ and a fixed $\alpha>1$, the probe set size M satisfies an inequality $Pr(\forall$code pairs, Hamming distance $\geq \alpha) > 1-\epsilon$.

19. (Original) The method of claim 15, wherein the threshold ρ has a value to enable the graph G to have a sparsity bounded by $A \leq$ sparsity $\leq B$, wherein the sparsity is definable by the average degree of a vertex in the graph G.

20. (Original) The method of claim 19, wherein the lower bound A is a relatively small constant, and the upper bound B is a function of the number of vertices n.

21. (Original) A software arrangement which, when executed on a processing device, configures the processing device to perform the steps comprising:

i) hybridizing the DNA sample to one or more microarrays to create a hybridization pattern, the one or more microarrays including a set of oligonucleotide probes that are capable of detecting at least one set of genotypes and haplotypes for a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample; and

ii) determining at least one of a genotype and a haplotype or a strain variant based on the hybridization pattern.

Claims 22-40 (Canceled).

41. (Original) A storage medium which includes thereon a software arrangement for providing one or more microarrays, which is capable of configuring a processing arrangement to perform the steps comprising:

i) receiving information regarding a hybridization of the DNA sample to one or more microarrays to create a hybridization pattern, the one or more microarrays including a set of oligonucleotide probes that are capable of detecting at least one set of genotypes and haplotypes for a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample; and

ii) determining at least one of a genotype and a haplotype or a strain variant based on the hybridization pattern.

Claims 42-60 (Canceled).

61. (Original) A system for at least one of genotyping and haplotyping polymorphic genetic loci or strain identification in a deoxyribonucleic acid (DNA) sample, comprising:

a processing arrangement which is capable of being programmed to:

i) receive information regarding a hybridization of the DNA sample to one or more microarrays to create a hybridization pattern, the one or more microarrays including a set of oligonucleotide probes that are capable of detecting at least one set of genotypes and haplotypes for a sequence of polymorphic genetic loci in a deoxyribonucleic acid (DNA) sample or identifying a strain variant from the DNA sample; and

ii) determine at least one of a genotype and a haplotype or a strain variant based on the hybridization pattern.

Claims 62-80 (Canceled).

81. (New) The method according to claim 4, wherein the match and mismatch criteria are the following:

$$\min \sum_{type\ j} w_j \ E\left[\Pi_{T_j \neq \hat{T}_j}\right]$$
$$\Leftrightarrow \ \min \sum_{type\ j} w_j \ \Pr\left(T_j \neq \hat{T}_j\right).$$

wherein T_j is a true allele contained in the DNA sample, $\hat{T}_j$ is the allele determined by the hybridization step, $\Pi_X = \begin{cases} 1, & \text{if } X \text{ is true} \\ 0, & \text{otherwise} \end{cases}$, and w_j is a weight assigned to at least one of the genotype and the haplotype *j*